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Five new species of Schizoporaceae (Basidiomycota, Hymenochaetales) from East Asia

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Abstract

Five new wood-inhabiting fungi, *Lyomyces albopulverulentus*, *L. yunnanensis*, *Xylodon daweishanensis*, *X. fissuratus*, and *X. puerensis* **spp. nov.**, are proposed based on a combination of morphological features and molecular evidence. *Lyomyces albopulverulentus* is characterized by brittle basidiomata, pruinose hymenophore with a white hymenial surface, a monomitic hyphal system with clamped generative hyphae, and ellipsoid basidiospores. *Lyomyces yunnanensis* is characterized by a grandinioid hymenial surface, the presence of capitate cystidia, and ellipsoid basidiospores. *Xylodon daweishanensis* is characterized by an odontioid hymenial surface, a monomitic hyphal system with clamped generative hyphae, and broad ellipsoid-to-subglobose basidiospores. *Xylodon fissuratus* is characterized by a cracking basidiomata with a grandinioid hymenial surface, and ellipsoid basidiospores. *Xylodon puerensis* is characterized by a poroid hymenophore with an angular or slightly daedaleoid configuration, and ellipsoid-to-broad-ellipsoid basidiospores. Sequences of ITS and nLSU rRNA markers of the studied samples were generated and phylogenetic analyses were performed with the maximum likelihood, maximum parsimony, and Bayesian inference methods. The phylogram based on the ITS+nLSU rDNA gene regions (Fig. 1) included six genera within the families Chaetoporellaceae, Hyphodontiaceae, Hymenochaetaceae, and Schizoporaceae (Hymenochaetales)—*Fasciodontia*, *Hastodontia*, *Hyphodontia*, *Kneiffiella*, *Lyomyces*, and *Xylodon*—in which the five new species were grouped into genera *Lyomyces* and *Xylodon*. The phylogenetic tree inferred from the ITS sequences highlighted that *Lyomyces albopulverulentus* formed a monophyletic lineage and was then grouped closely with *L. bambusinus*, *L. orientalis*, and *L. sambuci*; additionally, *L. yunnanensis* was sister to *L. niveus* with strong supports. The topology, based on the ITS sequences, revealed that *Xylodon daweishanensis* was retrieved as a sister to *X. hyphodontinus*; *X. fissuratus* was grouped with the four taxa *X. montanus*, *X. subclavatus*, *X. wenshanensis*, and *X. xinpingensis*; and *X. puerensis* was clustered with *X. flaviporus*, *X. ovisporus*, *X. subflaviporus*, *X. subtropicus*, and *X. taiwanianus*.

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Keywords
Biodiversity, China, molecular systematics, taxonomy, wood-inhabiting fungi, Yunnan Province

Introduction

Fungi represent one of the most diverse groups of organisms on the earth, with an indispensable role in the processes and functioning of ecosystems (Hyde 2022). The family Schizoporaceae Jülich includes many variations of the fruiting body types among the order Hymenochaetales Oberw. (Larsson et al. 2006; Wu et al. 2022a), in which it comprises many representative wood-inhabiting fungal taxa, including hydnoid, corticioid, and polyporoid basidiomes with diverse hymenophoral and cystidial morphology (Yurchenko and Wu 2016; Riebesehl and Langer 2017; Yurchenko et al. 2017; Cui et al. 2019; Riebesehl et al. 2019; Jiang et al. 2021; Wu et al. 2022a, b). In addition, the species of Schizoporaceae have been described from different countries, and they cause a white rot (Langer 1994).

The genus *Lyomyces* P. Karst. is a small corticioid group, typified by *L. sambuci* (Pers.) P. Karst. It is characterized by the resupinate-to-effused basidiomata with a smooth-to-odontioid hymenophore, a monomitic hyphal system with generative hyphae bearing clamp connections, the presence of several types of cystidia, and with smooth, thin- to slightly thick-walled basidiospores (Karsten 1881; Bernicchia and Gorjón 2010). The species of *Lyomyces* are found on fallen angiosperm branches, dead woody or herbaceous stems, or, occasionally, on gymnosperm wood (Yurchenko et al. 2017). Approximately 40 species of *Lyomyces* are currently known (Rabenhorst 1851; Karsten 1881, 1882; Cunningham 1959, 1963; Wu 1990; Hjortstam and Ryvarden 2009; Xiong et al. 2009; Dai 2010, 2011; Yurchenko et al. 2013, 2017, 2020; Gafforov et al. 2017; Riebesehl and Langer 2017; Chen and Zhao 2020; Luo et al. 2021b, c; Viner et al. 2022). The genus *Xylodon* (Pers.) Gray is typified by *X. quercinus* (Pers.) Gray (Bernicchia and Gorjón 2010). The taxa of this genus grow on rotten gymnosperm or angiosperm trunks and stumps, bamboo and ferns (Girometta et al. 2020; Greslebin and Rajchenberg 2000; Kotiranta and Saarenoksa 2000). They are characterized by resupinate or effuse basidiomata with a smooth, tuberculate, grandinioid, odontioid, coralloid, irpicoid, or poroid hymenophore; a monomitic or dimitic hyphal system with clamped generative hyphae; the presence of different types of cystidia, i.e., utriform or suburniform basidia; and cylindrical-to-ellipsoid-to-globose basidiospores, which can cause a white rot (Gray 1821; Bernicchia and Gorjón 2010). Based on the MycoBank database (http://www.mycobank.org, accessed on 24 December 2022) and the Index Fungorum (http://www.indexfungorum.org, accessed on 24 December 2022), *Xylodon* has registered 221 specific and infraspecific names, and the actual number of the species has reached 100 species (Chevallier 1826; Kuntze 1898; Wu 1990, 2000, 2001, 2006; Hjortstam and Ryvarden 2007, 2009; Xiong et al. 2009, 2010; Bernicchia and Gorjón 2010; Tura et al. 2011; Dai 2012; Lee and Langer 2012;

Yurchenko et al. 2013; Yurchenko and Wu 2014; Zhao et al. 2014; Chen et al. 2016; Kan et al. 2017a, b; Riehl and Langer 2017; Wang and Chen 2017; Viner et al. 2018, 2022; Riebesehl et al. 2019; Shi et al. 2019; Dai et al. 2021; Luo et al. 2021a, 2022; Qu and Zhao 2022; Qu et al. 2022).

Classification of the kingdom of fungi has been updated continuously, based on the frequent inclusion of data from DNA sequences in many phylogenetic studies (Wijayawardene et al. 2020). Based on the early embrace of molecular systematics by mycologists, both the discovery and classification of fungi, among the more basal branches of the tree, are now coming to light from genomic analyses and environmental DNA surveys that have been conducted (James et al. 2020). *Hyphodontia* s.l. was indicated to be a polyphyletic group, and *Xylodon* and *Kneiffiella* P. Karst. included the most species (Yurchenko and Wu 2016; Riebesehl and Langer 2017; Riebesehl et al. 2019). Given the lack of sequences for a part of the fungal taxa, it is difficult to clearly separate the many genera in this group using molecular data; therefore, a broad concept of *Hyphodontia* s.l. was accepted (Yurchenko and Wu 2016; Riebesehl and Langer 2017; Wang and Chen 2017; Riebesehl et al. 2019). On the basis of the nuclear DNA sequence data, six well-distinguished clades—*Lagarobasidium* clade, *Kneiffiella-Alutaceodontia* clade, *Hyphodontia* clade, *Hastodontia* clade, *Xylodon-Lyomyces*, *Rogersella* clade, and *Xylodon-Schizopora-Palifer* clade—were included based on the phylogenetical studies for *Hyphodontia* s.l., in which the genera *Xylodon* and *Lyomyces* were nested within the *Xylodon-Lyomyces-Rogersella* clade and *Xylodon-Schizopora-Palifer* clade, respectively (Yurchenko and Wu 2013). Riebesehl and Langer (2017) revealed that *Hyphodontia* s.l. was divided into six genera, viz., *Hastodontia* (Parmasto) Hjortstam & Ryvarden, *Hyphodontia* J. Erikss, *Kneiffiella*, *Lagarobasidium* Jülich, *Lyomyces*, and *Xylodon*, in which 35 new combinations were proposed, including fourteen *Lyomyces* species. Yurchenko et al. (2017) clarified the *Lyomyces sambuci* complex on the basis of the sequences of the internal transcribed spacer (ITS) and the nuclear large subunit (nLSU) ribosomal DNA gene, in which four new species were described. To confirm the taxonomic relationship of *Xylodon* species, Viner et al. (2018) proposed two genera, *Lagarobasidium* and *Xylodon*, which should be synonymous based on molecular data from the ITS and nLSU regions, and in which the three species were combined into *Xylodon*. Riebesehl et al. (2019) clarified the generic concept and their phylogenetic reconstruction of *Lyomyces*, in which *L. sambuci* was sister to *L. crustosus* (Pers.) P. Karst. Based on a combination of morphological and molecular evidence, the wood-inhabiting fungal diversity within the family Schizoporaceae of the order Hymenochaetales were analyzed, including *Lyomyces fissuratus* C.L. Zhao, *L. fumosus* C.L. Zhao, *L. niveus* C.L. Zhao and *L. ochraceoalbus* C.L. Zhao. (Luo et al. 2021b, 2021c). Viner et al. (2022) described three new species from Africa as *Xylodon angustisporus* Viner & Ryvarden, *X. dissiliens* Viner & Ryvarden, and *X. laxiusculus* Viner & Ryvarden, based on the morphological descriptions and molecular analyses that they conducted. A phylogenetic and taxonomic study on *Xylodon* showed that three new species of *Xylodon* were from southern China; in addition, it was also found that it enriched the fungal diversity of these areas (Qu et al. 2022).

During investigations on the wood-inhabiting fungi in the Yunnan–Guizhou Plateau of China, samples representing five additional species belonging to genera *Lyomyces* and *Xylodon* were collected. To clarify the placement and relationships of the five species, we carried out a phylogenetic and taxonomic study on *Lyomyces* and *Xylodon*, based on the ITS and nLSU sequences.

Materials and methods

Morphology

The studied specimens were deposited at the Herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. Macromorphological descriptions are based on field notes and photos captured in the field and lab. Color terminology follows Petersen (Petersen 1996). Micromorphological data were obtained from the dried specimens when observed under a light microscope following Dai (2012). The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB = Cotton Blue, CB– = acyanophilous, IKI = Melzer's Reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied and n = a/b (number of spores (a) measured from given number (b) of specimens).

Molecular phylogeny

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from the dried specimens following the manufacturer's instructions (Zhao and Wu 2017). The nuclear ribosomal ITS region was amplified with the primers ITS5 and ITS4 (White et al. 1990). The nuclear ribosomal LSU gene was amplified with the primers LR0R and LR7 (Vilgalys and Hester 1990; Rehner and Samuels 1994). The PCR procedure for ITS and nLSU followed previous study (Zhao and Wu 2017). All newly-generated sequences were deposited in NCBI GenBank (Table 1).

The sequences were aligned in MAFFT version 7 (Katoh et al. 2019) using the G-INS-i strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). Each dataset was aligned separately at first and then the ITS and nLSU regions were combined with Mesquite version 3.51. The combined dataset was deposited in TreeBASE (submission ID 29868). Sequences of *Hymenochaete ochromarginata* P.H.B. Talbot and *H. rubiginosa* (Dicks.) Lév. retrieved from GenBank were used as an outgroup in the ITS+nLSU analysis (Fig. 1); Sequences of *Xylodon quercinus* and *X. ramicida* Spirin & Miettinen retrieved from GenBank were used as an outgroup in the ITS analysis (Fig. 2); *Lyomyces bambusinus* C.L. Zhao and *L. sambuci* were selected as outgroup (Fig. 3) as inspired by a previous study (Luo et al. 2021c).

Table 1. List of species, specimens and GenBank accession numbers of sequences used in this study.

Species name	Specimen No.	GenBank accession No.		Country	References
		ITS	*nLSU*		
Fasciodontia brasiliensis	MSK-F 7245a	MK575201	MK598734	Brazil	Yurchenko et al. 2020
F. bugellensis	KAS-FD 10705a	MK575203	MK598735	France	Yurchenko et al. 2020
	MSK-F 7353	MK575205	MK598736	Belarus	Yurchenko et al. 2020
F. yunnanensis	CLZhao 6280	MK811275	MZ146327	China	Luo and Zhao 2021
	CLZhao 6385	MK811277	–	China	Luo and Zhao 2021
Hastodontia halonata	HHB-17058	MK575207	MK598738	Mexico	Yurchenko et al. 2020
Hymenochaete ochromarginata	He 47	KU978861	JQ279666	China	Unpublished
H. rubiginosa	He 458	JQ279580	–	China	He and Li 2013
Hyphodontia arguta	KHL 11938 (GB)	EU118632	EU118633	Sweden	Larsson 2007
H. pallidula	GEL 2097	DQ340317	DQ340372	Germany	Unpublished
H. zhixiangii	LWZ 20160909-4	KY440396	–	Uzbekistan	Kan et al. 2017
	LWZ 20160909-9	KY440398	–	Uzbekistan	Kan et al. 2017
Kneiffiella eucalypticola	LWZ20180515-9	MT319411	MT319143	Australia	Wang et al. 2021
K. palmae	GEL3456	DQ340333	DQ340369	China	Yurchenko et al. 2020
K. subalutacea	GEL2196	DQ340341	DQ340362	Norway	Yurchenko et al. 2020
Lyomyces albopulverulentus	**CLZhao 21478***	**OP730712**	**OP730724**	**China**	**Present study**
L. allantosporus	KAS-GEL4933	KY800401	–	France	Yurchenko et al. 2017
	FR-0249548	KY800397	–	La Réunion	Yurchenko et al. 2017
L. bambusinus	CLZhao 4831	MN945968	–	China	Chen and Zhao 2020
	CLZhao 4808	MN945970	–	China	Chen and Zhao 2020
	CLZhao 4831	MN945968	–	China	Chen and Zhao 2020
L. cremeus	CLZhao 4138	MN945974	–	China	Chen and Zhao 2020
	CLZhao 8295	MN945972	–	China	Chen and Zhao 2020
L. crustosus	TASM:YG G39	MF382993	–	Uzbekistan	Gafforov et al. 2017
	UC2022841	KP814310	–	USA	Unpublished
L. densiusculus	Ryvarden 44818	OK273853	–	Uganda	Viner et al. 2022
L. elaeidicola	LWZ20180411-20	MT319458	–	Malaysia	Wang et al. 2021
	LWZ20180411-19	MT319457	–	Malaysia	Wang et al. 2021
L. erastii	TASM:YG 022	MF382992	–	Uzbekistan	Gafforov et al. 2017
	23cSAMHYP	JX857800	–	Spain	Unpublished
L. fimbriatus	Wu910620-7	MK575209	–	China	Yurchenko et al. 2020
	Wu911204-4	MK575210	–	China	Yurchenko et al. 2020
L. fissuratus	CLZhao 4352	MW713742	–	China	Luo et al. 2021a
	CLZhao 4291	MW713738	–	China	Luo et al. 2021a
L. fumosus	CLZhao 8188	MW713744	–	China	Luo et al. 2021a
L. gatesiae	LWZ20180515-3	MT319447	–	Australia	Wang et al. 2021
	LWZ20180515-32	MT319448	–	Australia	Wang et al. 2021
L. griseliniae	KHL 12971 (GB)	DQ873651	–	Costa Rica	Larsson et al. 2006
L. juniperi	FR-0261086	KY081799	–	La Réunion	Riebesehl and Langer 2017
L. leptocystidiatus	LWZ20170818-1	MT326514	–	China	Wang et al. 2021
	LWZ20170818-2	MT326513	–	China	Wang et al. 2021
L. macrosporus	CLZhao 4516	MN945977	–	China	Chen and Zhao 2020
L. mascarensis	KAS-GEL4833	KY800399	–	La Réunion	Yurchenko et al. 2020
	KAS-GEL4908	KY800400	–	La Réunion	Yurchenko et al. 2020
L. microfasciculatus	CLZhao 5109	MN954311	–	China	Chen and Zhao 2020
L. niveus	CLZhao 6431	MZ262541	MZ262526	China	Luo et al. 2021b
	CLZhao 6442	MZ262542	MZ262527	China	Luo et al. 2021b
L. ochraceoalbus	CLZhao 4385	MZ262535	MZ262521	China	Luo et al. 2021b
	CLZhao 4725	MZ262536	MZ262522	China	Luo et al. 2021b
L. organensis	MSK7247	KY800403	–	Brazil	Yurchenko et al. 2017
L. orientalis	GEL3376	DQ340325	–	China	Yurchenko et al. 2017

Species name	Specimen No.	GenBank accession No.		Country	References
		ITS	*nLSU*		
L. pruni	GEL2327	DQ340312	–	Germany	Larsson et al. 2006
	Ryberg 021018 (GB)	DQ873624	–	Sweden	Larsson et al. 2006
L. sambuci	KAS-JR7	KY800402	KY795966	Germany	Yurchenko et al. 2017
	83SAMHYP	JX857721	–	USA	Yurchenko et al. 2017
L. vietnamensis	TNM F9073	JX175044	–	Vietnam	Yurchenko et al. 2013
L. wuliangshanensis	CLZhao 4108	MN945980	–	China	Chen and Zhao 2020
	CLZhao 4167	MN945979	–	China	Chen and Zhao 2020
L. yunnanensis	**CLZhao 2463**	**OP730711**	**OP730723**	**China**	**Present study**
	CLZhao 9375	**OP730710**	**–**	**China**	**Present study**
	CLZhao 10041*	**OP730709**	**–**	**China**	**Present study**
Xylodon acystidiatus	LWZ20180514-9	MT319474	–	Australia	Wang et al. 2021
X. apacheriensis	Wu 0910-58	KX857797	–	China	Chen et al. 2017
X. aspera	KHL 8530	AY463427	–	Sweden	Larsson et al. 2004
X. astrocystidiata	Wu 9211-71	JN129972	–	China	Yurchenko and Wu 2014
X. attenuatus	Spirin 8775	MH324476	–	America	Viner et al. 2018
X. australis	LWZ20180509-8	MT319503	–	China	Wang et al. 2021
X. bambusinus	CLZhao 9174	MW394657	–	China	Ma and Zhao 2021
X. borealis	JS26064	AY463429	–	Norway	Larsson et al. 2004
X. brevisetus	JS17863	AY463428	–	Norway	Larsson et al. 2004
X. crystalliger	LWZ20170816-33	MT319521	–	China	Wang et al. 2021
X. cystidiatus	FR-0249200	MH880195	MH884896	Réunion	Riebesehl et al. 2019
X. damansaraensis	LWZ20180417-23	MT319499	–	Malaysia	Wang et al. 2021
X. daweishanensis	**CLZhao 18357***	**OP730715**	**–**	**China**	**Present study**
	CLZhao 18425	**OP730716**	**–**	**China**	**Present study**
	CLZhao 18446	**OP730717**	**OP730725**	**China**	**Present study**
	CLZhao 18458	**OP730718**	**OP730726**	**China**	**Present study**
	CLZhao 18492	**OP730719**	**OP730727**	**China**	**Present study**
X. detriticus	Zíbarová 30.10.17	MH320793	–	Czech Republic	Viner et al. 2018
X. filicinus	MSK-F 12869	MH880199	NG067836	China	Riebesehl et al. 2019
X. fissuratus	**CLZhao 9407***	**OP730714**	**–**	**China**	**Present study**
	CLZhao 7007	**OP730713**	**–**	**China**	**Present study**
X. flaviporus	FR-0249797	MH880201	–	Réunion	Riebesehl et al. 2019
X. flocculosus	CLZhao 18342	MW980776	–	China	Qu and Zhao 2022
X. follis	FR-0249814	MH880204	–	Réunion	Riebesehl et al. 2019
X. gossypinus	CLZhao 8375	MZ663804	MZ663813	China	Luo et al. 2021
X. grandineus	CLZhao 16075	OM338091	–	China	Luo et al. 2022
	CLZhao 6425	OM338090	–	China	Luo et al. 2022
X. hastifer	K(M) 172400	NR166558	–	USA	Riebesehl and Langer 2017
X. heterocystidiatus	Wei 17-314	MT731753	–	China	Unpublished
X. hyphodontinus	KAS-GEL9222	MH880205	MH884903	Kenya	Riebesehl et al. 2019
X. kunmingensis	TUB-FO 42565	MH880198	–	China	Riebesehl et al. 2019
X. lacerates	CLZhao 9892	OL619258	–	China	Qu et al. 2022
X. lagenicystidiatus	LWZ20180513-16	MT319634	–	Australia	Wang et al. 2021
X. lenis	Wu890714-3	KY081802	–	China	Riebesehl and Langer 2017
X. macrosporus	CLZhao 10226	MZ663809	MZ663817	China	Luo et al. 2021
X. mollissimus	LWZ 20160318-3	KY007517	–	China	Wang et al. 2021
X. montanus	CLZhao 8179	OL619260	–	China	Qu et al. 2022
X. nespori	LWZ20180921-35	MT319655	MT319238	China	Wang et al. 2021
X. niemelaei	LWZ20150707-13	MT319630	–	China	Wang et al. 2021
X. nongravis	GC 1412-22	KX857801	–	China	Chen et al. 2017
X. nothofagi	ICMP 13842	AF145583	–	China	Paulus et al. 2000
X. ovisporus	LWZ20170815-31	MT319666	–	China	Wang et al. 2021
X. papillosa	CBS:114.71	MH860026	–	Netherlands	Vu et al. 2019

Species name	Specimen No.	GenBank accession No.		Country	References
		ITS	*nLSU*		
X. paradoxus	Dai14983	MT319519	–	China	Wang et al. 2021
X. pruinosus	Spirin 2877	MH332700	–	Estonia	Viner et al. 2018
X. pseudolanatus	CFMR FP-150922	MH880220	–	Belize	Riebesehl et al. 2019
X. pseudotropicus	Dai16167	MT319509	–	China	Wang et al. 2021
X. puerensis	**CLZhao 8142***	**OP730720**	**OP730728**	**China**	**Present study**
	CLZhao 8639	**OP730721**	**OP730729**	**China**	**Present study**
X. punctus	CLZhao 17691	OM338092	–	China	Luo et al. 2022
X. quercinus	Larsson 11076 (GB)	KT361633	–	Sweden	Larsson et al. 2004
X. ramicida	Spirin 7664	NR138013	–	usa	Unpublished
X. rhododendricola	LWZ20180513-9	MT319621	–	Australia	Wang et al. 2021
X. rimosissima	Ryberg 021031 (GB)	DQ873627	–	Sweden	Larsson et al. 2006
X. serpentiformis	LWZ20170816-15	MT319673	–	China	Wang et al. 2021
X. sinensis	CLZhao 11120	MZ663811	–	China	Luo et al. 2021
X. spathulatus	LWZ20180804-10	MT319646	–	China	Wang et al. 2021
X. subclavatus	TUB-FO 42167	MH880232	–	China	Riebesehl et al. 2019
X. subflaviporus	Wu 0809-76	KX857803	–	China	Chen et al. 2017
X. subserpentiformis	LWZ20180512-16	MT319486	–	Australia	Wang et al. 2021
X. subtropicus	LWZ20180510-24	MT319541	–	China	Wang et al. 2021
X. taiwanianus	CBS:125875	MH864080	–	Netherlands	Vu et al. 2019
X. tropicus	CLZhao 3351	OL619261	OL619269	China	Qu et al. 2022
X. ussuriensis	KUN 1989	NR166241	–	USA	Unpublished
X. verecundus	KHL 12261 (GB)	DQ873642	–	Sweden	Larsson et al. 2006
X. victoriensis	LWZ20180510-29	MT319487	–	Australia	Wang et al. 2021
X. wenshanensis	CLZhao 10790	OM338095	–	China	Luo et al. 2022
	CLZhao 15729	OM338097	OM338104	China	Luo et al. 2022
X. xinpingensis	CLZhao 11224	MW394662	MW394654	China	Luo et al. 2022
X. yarraensis	LWZ20180510-5	MT319639	–	Australia	Wang et al. 2021
X. yunnanensis	LWZ20180922-47	MT319660	–	China	Wang et al. 2021

* Indicates type materials.

Maximum parsimony analysis in PAUP* version 4.0a169 (http://phylosolutions.com/paup-test/) was applied to ITS and the combined ITS+nLSU datasets following a previous study (Zhao and Wu 2017). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1,000 random sequence additions. Max-trees were set to 5,000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 pseudo replicates (Felsenstein 1985). Descriptive tree statistics – tree length (TL), composite consistency index (CI), composite retention index (RI), composite rescaled consistency index (RC) and composite homoplasy index (HI) – were calculated for each maximum parsimonious tree generated. The combined dataset was also analysed using Maximum Likelihood (ML) in RAxML-HPC2 through the CIPRES Science Gateway (Miller et al. 2012). Branch support (BS) for the ML analysis was determined by 1000 bootstrap pseudoreplicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each dataset for the purposes of Bayesian inference (BI). which was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a

gamma distribution rate variation across sites (Ronquist et al. 2012). A total of four Markov chains were run for two runs from random starting trees for 8 million generations for ITS+nLSU (Fig. 1); 0.5 million generations for ITS (Fig. 2) and 9.5 million generations for ITS (Fig. 3) with trees and parameters sampled every 1,000 generations. The first quarter of all of the generations were discarded as burn-ins. A majority rule consensus tree was computed from the remaining trees. Branches were considered as significantly supported if they received a maximum likelihood bootstrap support value (BS) of > 70%, a maximum parsimony bootstrap support value (BT) of > 70% or a Bayesian posterior probability (BPP) of > 0.95.

Results

Molecular phylogeny

The ITS+nLSU dataset (Fig. 1) comprised sequences from 43 fungal specimens representing 31 taxa. The dataset had an aligned length of 2,100 characters, of which 1,323 characters were constant, 156 were variable and parsimony-uninformative and 621 (35%) were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 2,867, CI = 0.4423, HI = 0.5577, RI = 0.6488 and RC = 0.2869). The best model of nucleotide evolution for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was found to be GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as in the MP analysis. The Bayesian analysis had an average standard deviation of split frequencies = 0.008603 (BI) and the effective sample size (ESS) across the two runs is double the average ESS (avg. ESS) = 1,623. The phylogram based on the ITS+nLSU rDNA gene regions (Fig. 1) include six genera within Schizoporaceae (Hymenochaetales), which are *Fasciodontia*, *Hastodontia*, *Hyphodontia*, *Kneiffiella*, *Lyomyces*, and *Xylodon*—in which five new species were grouped into the genera *Lyomyces* and *Xylodon*.

The ITS dataset (Fig. 2) comprised sequences from 47 fungal specimens representing 29 taxa. The dataset had an aligned length of 661 characters, of which 316 characters were constant, 53 were variable and parsimony-uninformative and 292 (35%) were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 1,371, CI = 0.4136, HI = 0.5864, RI = 0.6984 and RC = 0.2888). The best model of nucleotide evolution for the ITS dataset estimated and applied in the Bayesian analysis was found to be GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as in the MP analysis. The Bayesian analysis had an average standard deviation of split frequencies = 0.006564 (BI) and the effective sample size (ESS) across the two runs is double the average ESS (avg. ESS) = 359. The phylogenetic tree (Fig. 2), inferred from the ITS sequences, highlighted that *L. albopulverulentus* formed a monophyletic lineage. It was then grouped closely with *L. bambusinus*, *L. orientalis* Riebesehl, Yurch. & Langer, and *L. sambuci*. In addition, *L. yunnanensis* was found to be the sister to *L. niveus* with strong supports.

Figure 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Xylodon*, *Lyomyces* and related genera in the order Hymenochaetales based on ITS+nLSU sequences. Branches are labelled with maximum likelihood bootstrap values > 70%, parsimony bootstrap values > 50% and Bayesian posterior probabilities > 0.95, respectively.

The ITS dataset (Fig. 3) comprised sequences from 72 fungal specimens representing 65 taxa. The dataset had an aligned length of 702 characters, of which 283 characters were constant, 96 were variable and parsimony-uninformative and 323 (35%) were parsimony-informative. Maximum parsimony analysis yielded 5,000 equally parsimonious trees (TL = 2,726, CI = 0.2748, HI = 0.7252, RI = 0.4280 and RC = 0.1176). The best model of nucleotide evolution for the ITS dataset estimated and applied in the Bayesian analysis was found to be GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as in the MP analysis. The Bayesian analysis had an average standard deviation of split frequencies = 0.02518 (BI) and the effective sample size (ESS) across the two runs is double the average ESS (avg. ESS) = 1,440. The topology (Fig. 3), based on ITS sequences, revealed that *X. daweishanensis* was retrieved as a sister to *X. hyphodontinus* (Hjortstam & Ryvarden) Riebesehl, Yurchenko & G. Gruhn. Furthermore, *X. fissuratus* was grouped with four taxa: *X. montanus* C.L. Zhao; *X. subclavatus* (Yurchenko, H.X. Xiong & Sheng H. Wu) Riebesehl, Yurch. &

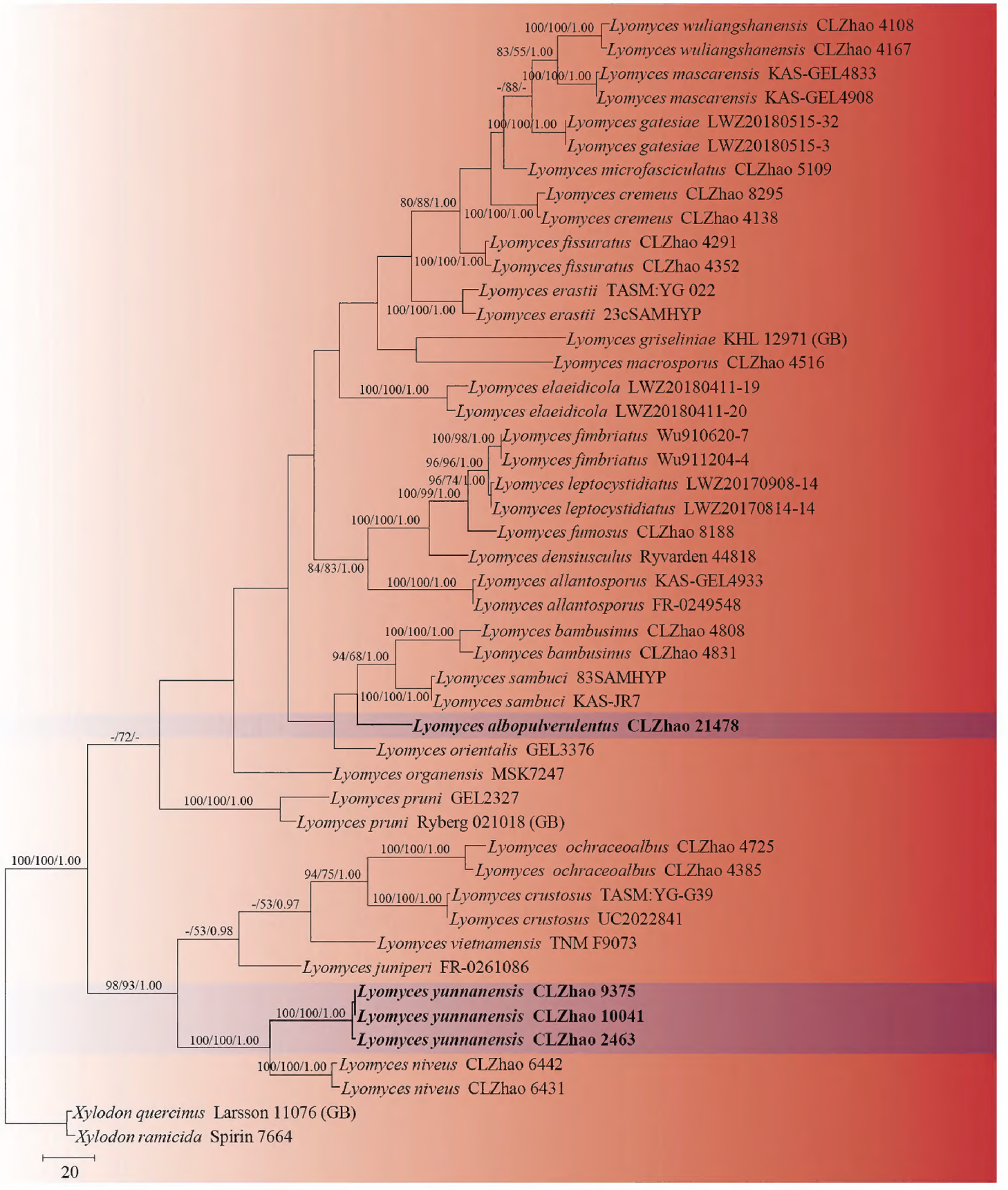

Figure 2. Maximum parsimony strict consensus tree illustrating the phylogeny of the two new species and related species in *Lyomyces*, based on ITS sequences. Branches are labelled with maximum likelihood bootstrap values > 70%, parsimony bootstrap values > 50% and Bayesian posterior probabilities > 0.95, respectively.

Langer; *X. wenshanensis* K.Y. Luo & C.L. Zhao; and *X. xinpingensis* C.L. Zhao & X. Ma. Moreover, *X. puerensis* was clustered with *X. flaviporus* (Berk. & M.A. Curtis ex Cooke) Riebesehl & Langer, *X. ovisporus* (Corner) Riebesehl & Langer, *X. subflaviporus* C.C. Chen & Sheng H. Wu, *X. subtropicus* (C.C. Chen & Sheng H. Wu) C.C. Chen & Sheng H. Wu, and *X. taiwanianus* (Sheng H. Wu) Hjortstam & Ryvarden.

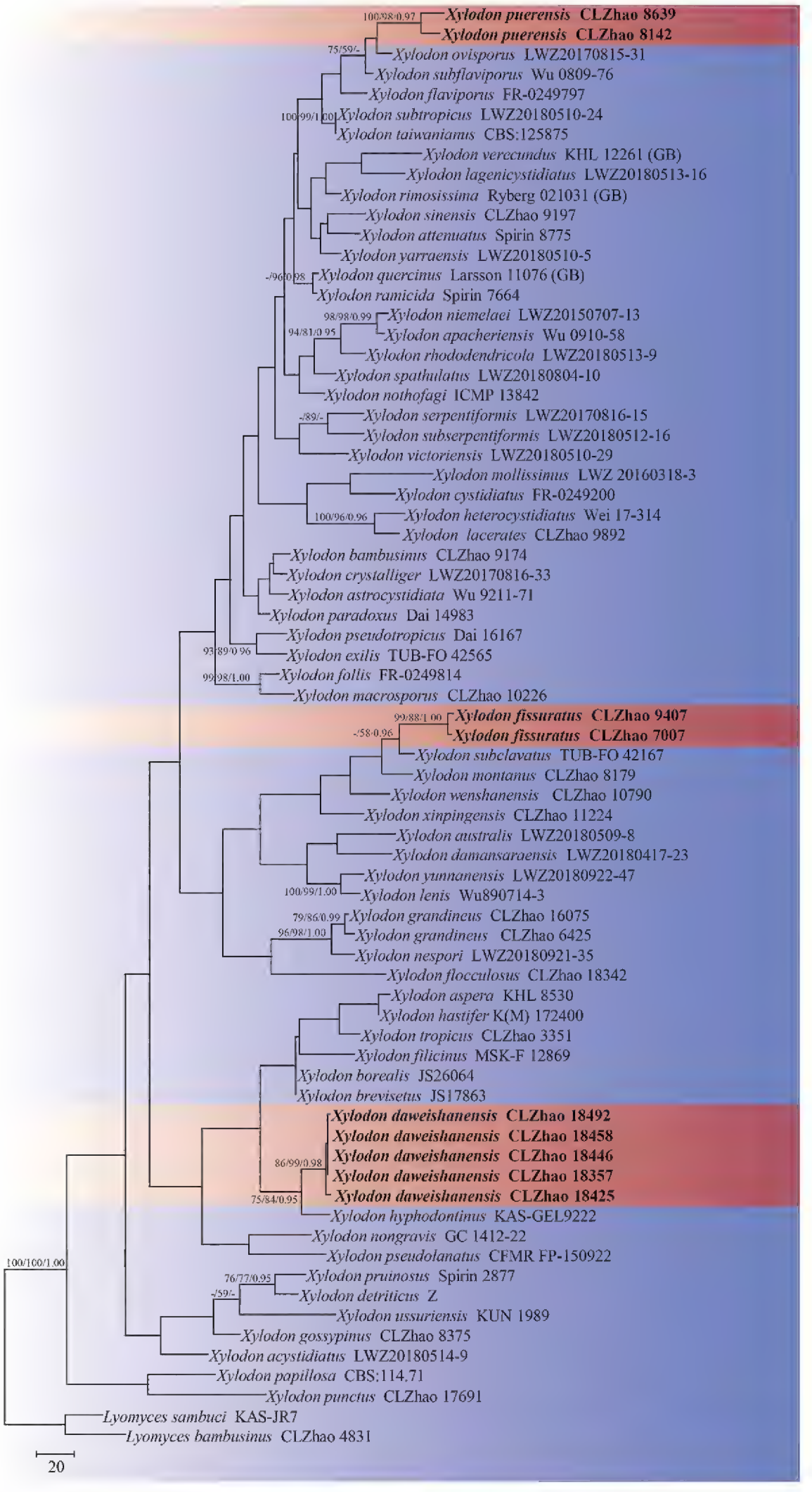

Figure 3. Maximum parsimony strict consensus tree illustrating the phylogeny of the three new species and related species in *Xylodon*, based on ITS sequences. Branches are labelled with maximum likelihood bootstrap values > 70%, parsimony bootstrap values > 50% and Bayesian posterior probabilities > 0.95, respectively.

Taxonomy

***Lyomyces albopulverulentus* C.L. Zhao, sp. nov.**
MycoBank No: 846525
Figs 4, 5

Type material. *Holotype.* China. Yunnan Province, Lijiang, Lashihai Nature Reserve, 26°51'37"N, 100°8'14"E, altitude 2450 m a.s.l., on fallen angiosperm branch, leg. C.L. Zhao, 19 July 2021, CLZhao 21478 (SWFC).

Etymology. *Albopulverulentus* (Lat.): referring to the white and pruinose hymenial surface.

Description. Basidiomata annual, resupinate, adnate, brittle, without odor or taste when fresh, up to 12 cm long, 1.5 cm wide, and 150 μm thick. Hymenial surface pruinose, white when fresh and drying. Sterile margin indistinct, white, and up to 2 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thick-walled, frequently branched, interwoven, 3.5–5.5 μm in diameter; IKI–, CB–, tissues unchanged in KOH; subhymenial hyphae densely covered by crystals.

Cystidia capitate, colorless, thin-walled, smooth, slightly constricted at the neck, with a globose tip, 37–54 × 5–9 μm; basidia clavate, slightly sinuous, with four sterigmata and a basal clamp connection, 24.5–28.5 × 7–9 μm.

Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (7.5–)8–10.5(–11) × (5–)5.5–7 μm, L =9.12 μm, W = 6 μm, Q = 1.52 (n = 30/1).

Additional specimen examined (paratype). China. Yunnan Province, Yuxi, Xinping County, the Ancient Tea Horse Road, 23°57'10"N, 101°30'41"E, altitude 2,600 m a.s.l., on fallen angiosperm branch, leg. C.L. Zhao, 13 January 2018, CLZhao 5234 (SWFC).

***Lyomyces yunnanensis* C.L. Zhao, sp. nov.**
MycoBank No: 846527
Figs 6, 7

Type material. *Holotype.* China. Yunnan Province, Dali, Nanjian County, Lingbaoshan, 24°46'2"N, 100°30'26"E, altitude 2350 m a.s.l., on fallen angiosperm branch, leg. C.L. Zhao, 9 January 2019, CLZhao 10041 (SWFC).

Etymology. *Yunnanensis* (Lat.): referring to the locality (Yunnan Province) of the type specimen.

Description. Basidiomata annual, resupinate, adnate, coriaceous when fresh, becoming farinaceous upon drying, without odor or taste when fresh, up to 15 cm long, 2.5 cm wide, and 150 μm thick. Hymenial surface grandinioid, cream to buff when fresh, and buff upon drying. Sterile margin indistinct, buff, and up to 1 mm wide.

Figure 4. Basidiomata of *Lyomyces albopulverulentus* (holotype). Scale bars: 2 cm (**A**); 1 mm (**B**).

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thick-walled, frequently branched, interwoven, 2.5–3 μm in diameter; IKI–, CB–, tissues unchanged in KOH. Numerous crystals present among hyphae.

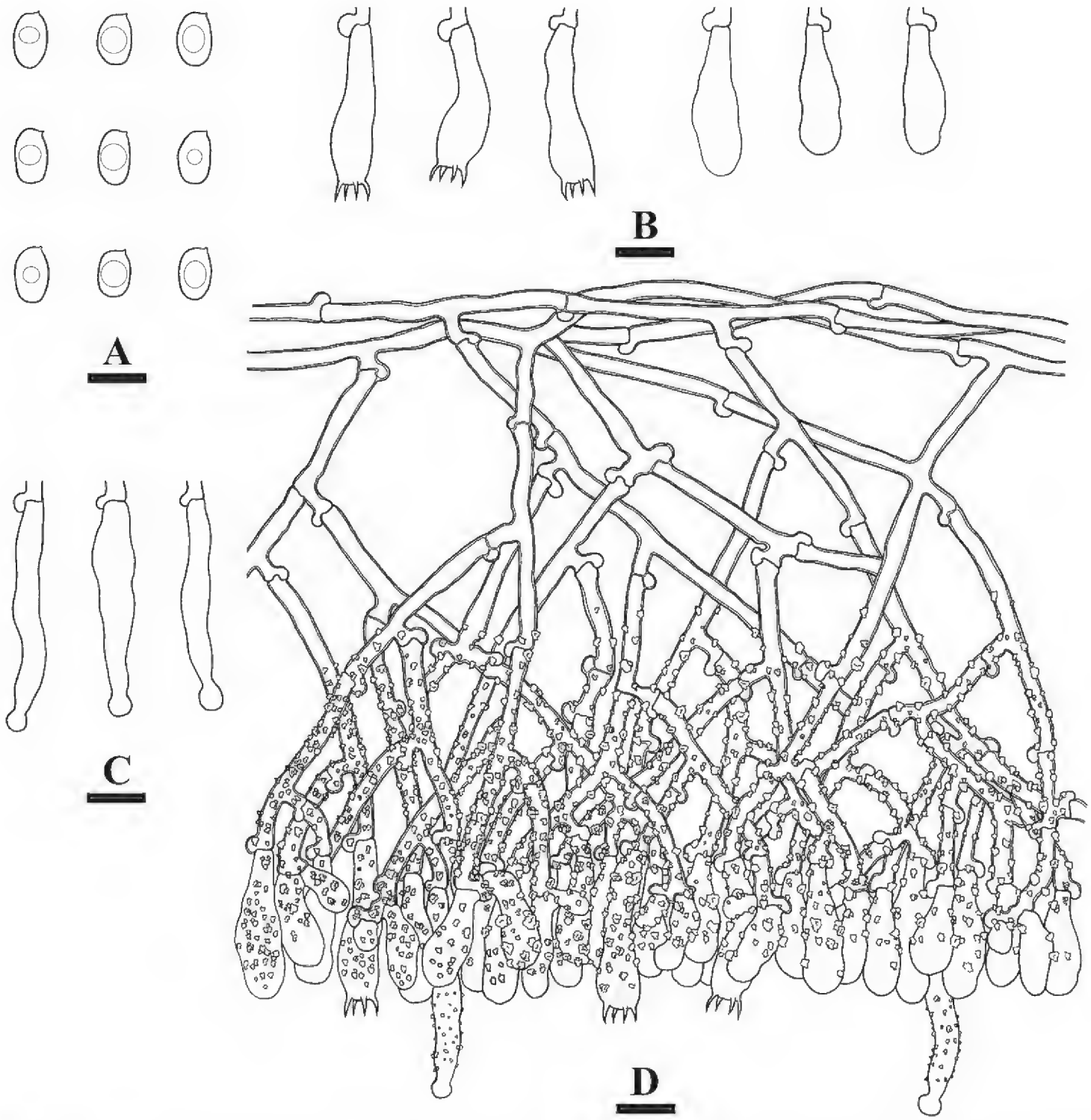

Figure 5. Microscopic structures of *Lyomyces albopulverulentus* (holotype) **A** basidiospores **B** basidia and basidioles **C** capitate cystidia **D** a section of hymenium. Scale bars: 10 μm (**A–D**).

Cystidia of two types: (1) fusiform, tapering, colorless, thin-walled, 18–39 × 4–6 μm; (2) capitate cystidia, colorless, thin-walled, 16–23.5 × 3–5 μm; fusoid cystidioles present, colorless, thin-walled, 18–25 × 3–6 μm; basidia clavate, slightly sinuous, with four sterigmata and a basal clamp connection, 16.5–27 × 4–5.5 μm.

Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (4.5–)5–7 × 3–4.5 μm, L = 5.72 μm, W = 3.6 μm, Q = 1.54–1.65 (n = 90/3).

Additional specimens examined (paratypes). China. Yunnan Province, Yuxi, Xinping County, Mopanshan National Forestry Park, 23°55'48"N, 101°59'22"E, altitude 2150 m a.s.l., on fallen angiosperm branch, leg. C.L. Zhao, 19 August 2017,

Figure 6. Basidiomata of *Lyomyces yunnanensis* (holotype). Scale bars: 2 cm (**A**); 1 mm (**B**).

CLZhao 2463 (SWFC); Puer, Jingdong County, the Forest of Pineapple, 24°21'32"N, 100°48'12"E, altitude 2110 m a.s.l., on fallen angiosperm branch, leg. C.L. Zhao, 4 January 2019, CLZhao 9375 (SWFC).

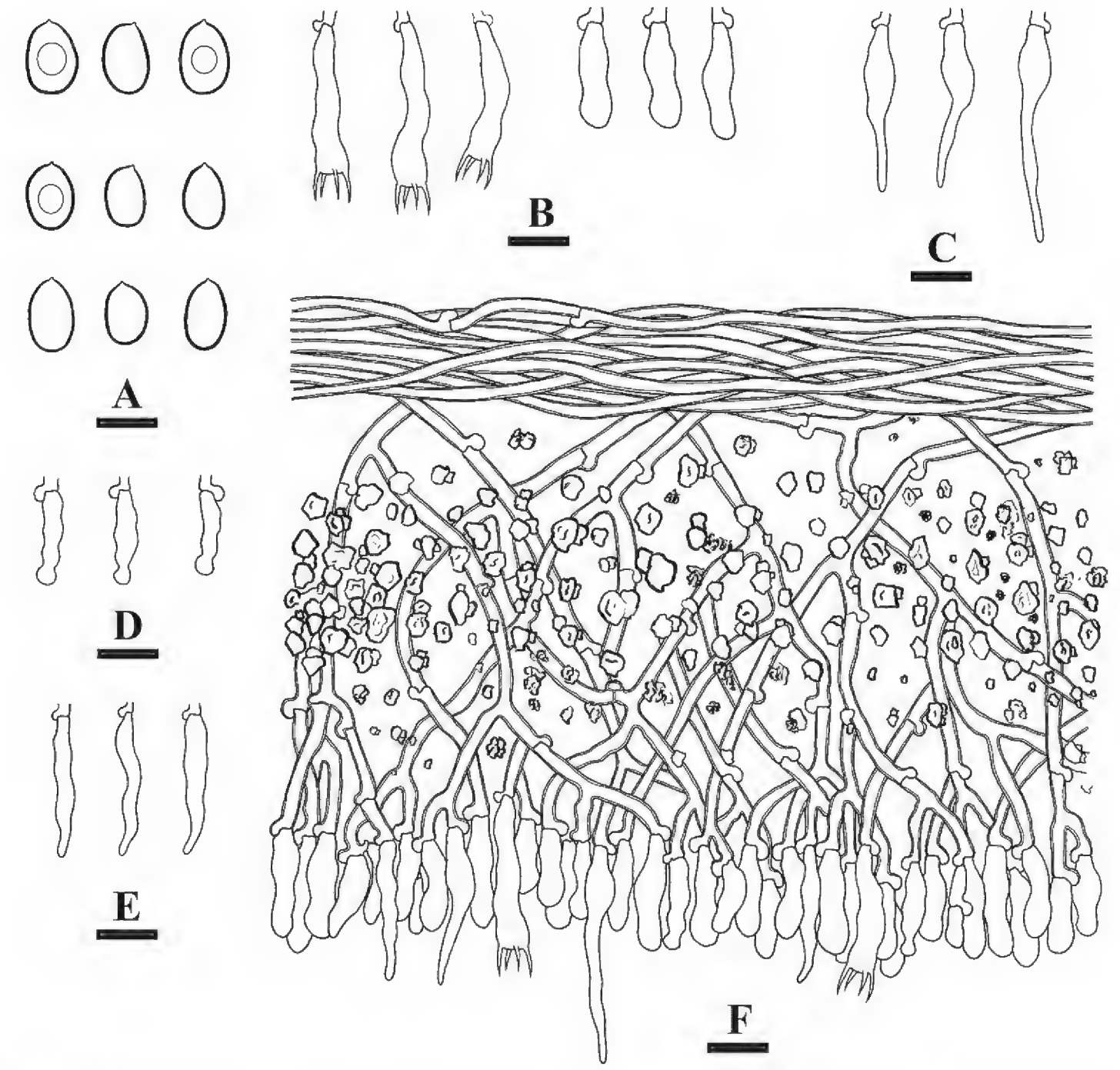

Figure 7. Microscopic structures of *Lyomyces yunnanensis* (holotype) **A** basidiospores **B** basidia and basidioles **C** tapering cystidia **D** capitate cystidia **E** fusoid cystidioles **F** a section of hymenium. Scale bars: 5 μm (**A**); 10 μm (**B–F**).

***Xylodon daweishanensis* C.L. Zhao, sp. nov.**
MycoBank No: 846530
Figs 8, 9

Type material. ***Holotype.*** China. Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, 22°53'26"N, 103°35'37"E, altitude 1990 m a.s.l., on angiosperm trunk, leg. C.L. Zhao, 3 August 2019, CLZhao 18357 (SWFC).

Etymology. *Daweishanensis* (Lat.): referring to the locality (Daweishan) of the type specimen.

Description. Basidiomata annual, resupinate, adnate, without odor or taste when fresh, coriaceous, up to 10 cm long, 5 cm wide, and 150 μm thick. Hymenial surface odontioid, slightly buff when fresh, and buff upon drying. Margin sterile, slightly buff, and 1 mm wide.

Figure 8. Basidiomata of *Xylodon daweishanensis* (holotype). Scale bars: 2 cm (**A**); 1 mm (**B**).

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin to thick-walled, frequently branched, interwoven, 1.5–4 μm in diameter, IKI–, CB–, tissues unchanged in KOH.

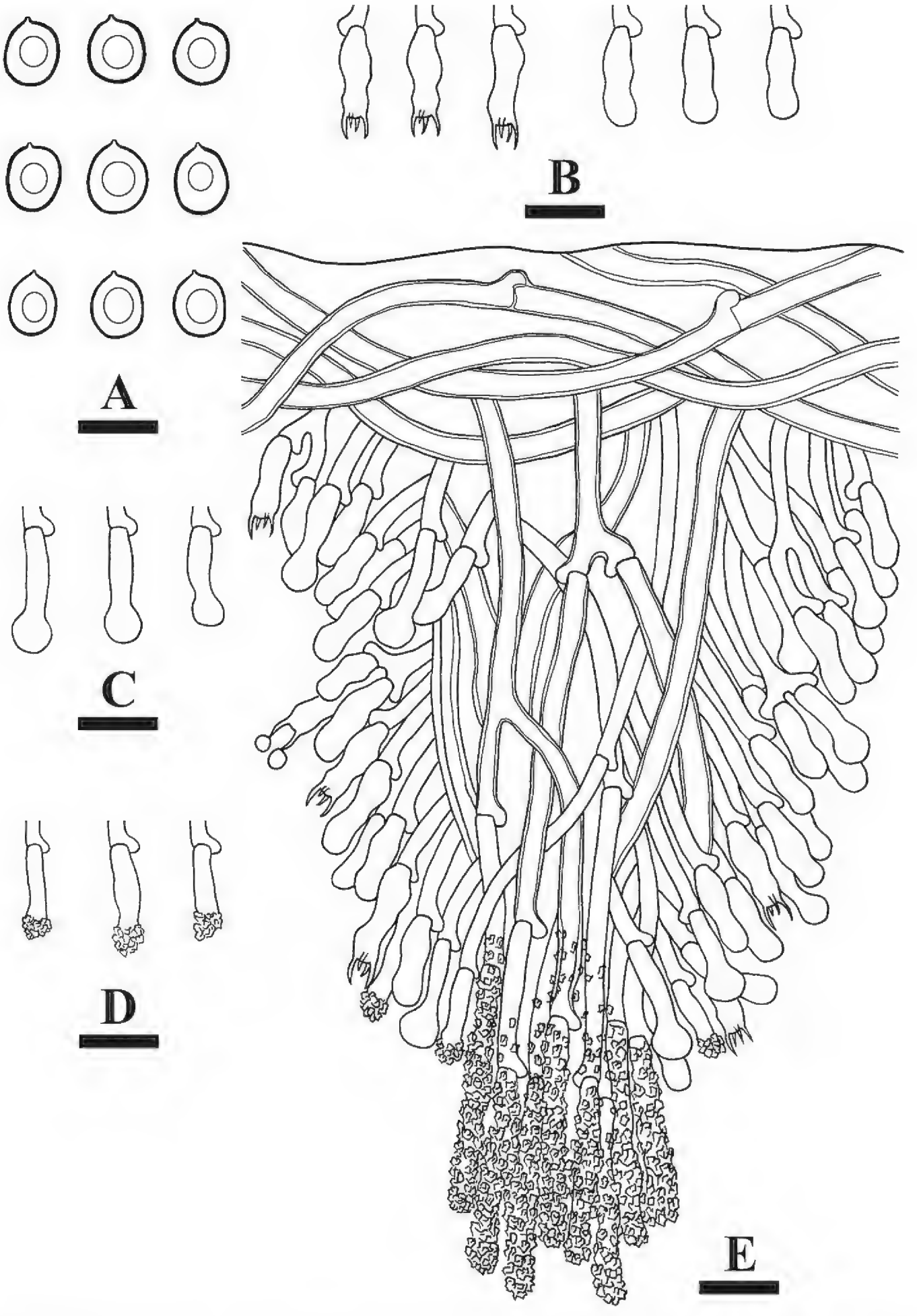

Figure 9. Microscopic structures of *Xylodon daweishanensis* (holotype) **A** basidiospores **B** basidia and basidioles **C** capitate cystidia **D** asterocystidia **E** a section of hymenium. Scale bars: 5 μm (**A**); 10 μm (**B–E**).

Cystidia of two types: (1) capitate cystidia thin-walled, smooth, slightly constricted at the neck, with a globose tip, 11–23.5 × 2.5–5 μm; (2) asterocystidia thin-walled, with the apical part encrusted, 11–26.5 × 2.5–4.5 μm; basidia clavate to subcylindrical,

constricted, somewhat sinuous, with four sterigmata and a basal clamp connection, 11–15.5 × 2.5–4 μm.

Basidiospores broad ellipsoid to subglobose, colorless, thin-walled, smooth, with oil drops, IKI–, CB–, 3–4 × 2.5–3.5(–4) μm, L = 3.51 μm, W = 3.14 μm, Q = 1.09–1.15 (n = 150/5).

Additional specimens examined (paratypes). China. Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, 22°53'26"N, 103°35'37"E, altitude 1990 m a.s.l., on angiosperm trunk, leg. C.L. Zhao, 3 August 2019, CLZhao 18425, CLZhao 18446, CLZhao 18458, and CLZhao 18492 (SWFC).

***Xylodon fissuratus* C.L. Zhao, sp. nov.**
MycoBank No: 846532
Figs 10, 11

Type material. *Holotype.* China. Yunnan Province, Puer, Jingdong County, the Forest of Pineapple, 24°21'32"N, 100°48'12"E, altitude 2110 m a.s.l., on fallen angiosperm branch, leg. C.L. Zhao, 4 January 2019, CLZhao 9407 (SWFC).

Etymology. *Fissuratus* (Lat.): referring to the cracking hymenial surface.

Description. Basidiomata annual, resupinate, adnate, coriaceous, without odor or taste when fresh, up to 12 cm long, 2.5 cm wide, and 150 μm thick. Hymenial surface grandinioid, and white when fresh, white to slightly cream on drying, cracking. Sterile margin indistinct, white, and up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 2–3 μm in diameter; IKI–, CB–, tissues unchanged in KOH.

Cystidia capitate, thin-walled, smooth, slightly constricted at the neck, with a globose tip, 11.5–16.5 × 3–4.5 μm; basidia clavate to subcylindrical, slightly constricted in the middle to somewhat sinuous, with four sterigmata and a basal clamp connection, 10.5–16.5 × 2–4 μm.

Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, 4–5 × 3–4 μm, L = 4.44 μm, W = 3.4 μm, Q = 1.3 (n = 30/1).

Additional specimen examined (paratype). China. Yunnan Province, Chuxiong, Zixishan Forestry Park, 25°01'26"N, 101°24'37"E, altitude 2313 m a.s.l., on fallen angiosperm branch, leg. C.L. Zhao, 1 July 2018, CLZhao 7007 (SWFC).

***Xylodon puerensis* C.L. Zhao, sp. nov.**
MycoBank No: 846533
Figs 12, 13

Type material. *Holotype.* China. Yunnan Province, Puer, Zhenyuan County, Heping Town, Jinshan Virgin Forest Park, 23°56'21"N, 101°25'32"E, altitude 2240 m a.s.l., on fallen angiosperm branch, leg. C.L. Zhao, 21 August 2018, CLZhao 8142 (SWFC).

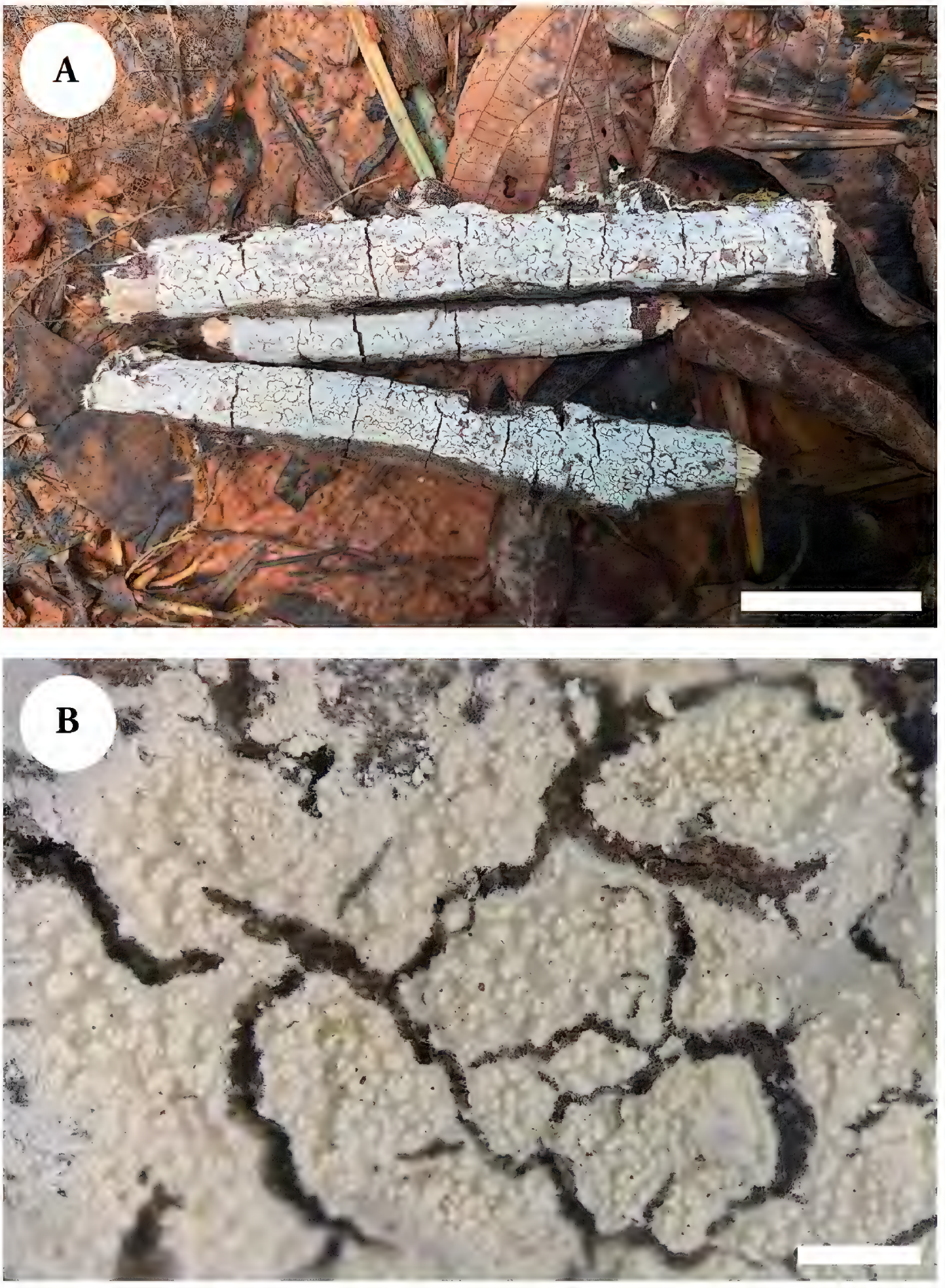

Figure 10. Basidiomata of *Xylodon fissuratus* (holotype). Scale bars: 2 cm (**A**); 1 mm (**B**).

Etymology. *Puerensis* (Lat.): referring to the locality (Yunnan Province) of the type specimen.

Description. Basidiomata annual, resupinate, adnate, coriaceous, without odor or taste when fresh, up to 12 cm long, 5 cm wide, and 200 μm thick. Hymenial surface

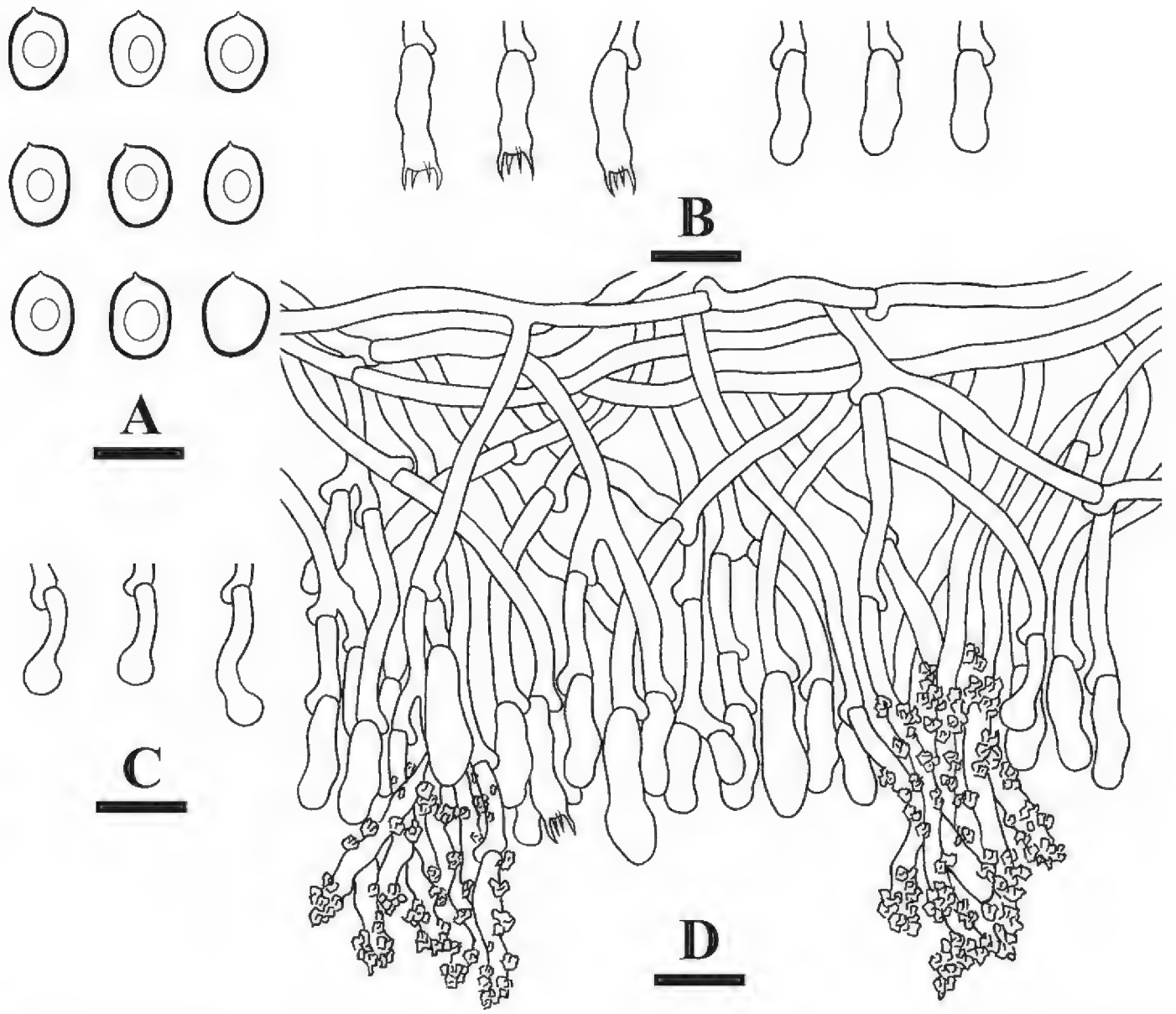

Figure 11. Microscopic structures of *Xylodon fissuratus* (holotype) **A** basidiospores **B** basidia and basidioles **C** capitate cystidia **D** a section of hymenium. Scale bars: 5 μm (**A**); 10 μm (**B–D**).

poroid, pores angular or slightly daedaleoid, 3–6 per mm, and cream when fresh, buff on drying. Sterile margin slightly buff, and up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamps, colorless, thick-walled, frequently branched, interwoven, 2.5–4.5 μm in diameter; IKI–, CB–, tissues unchanged in KOH.

Cystidia of four types: (1) paraphysoid cystidia colorless, smooth, 12–20.5 × 3–5 μm; (2) astrocystidia colorless, thin-walled, smooth, 9–11 × 3.5–5.5 μm; (3) capitate cystidia, colorless, thin-walled, smooth, embedded, 22–29.5 × 6.5–12 μm; (4) septocystidia, thin-walled, smooth, with the apical part encrusted, 32–51 × 3.5–6 μm; basidia clavate to subcylindrical, slightly sinuous or distinctly sinuous, with four sterigmata and a basal clamp connection, 14.5–20 × 5–7 μm.

Basidiospores ellipsoid to broad ellipsoid, colorless, thin-walled, smooth, with oil drops, IKI–, CB–, (5.5–)6–7 × 4.5–5.5 μm, L = 6.41 μm, W = 5.01 μm, Q = 1.28 (n = 30/1).

Additional specimen examined (paratype). China. Yunnan Province, Puer, Jingdong County, Taizhong Town, Ailaoshan Ecological Station, 24°29'41"N, 100°56'32"E, altitude 1930 m a.s.l., on angiosperm trunk, leg. C.L. Zhao, 24 August 2018, CLZhao 8639 (SWFC).

Figure 12. Basidiomata of *Xylodon puerensis* (holotype). Scale bars: 2 cm (**A**); 1 mm (**B**).

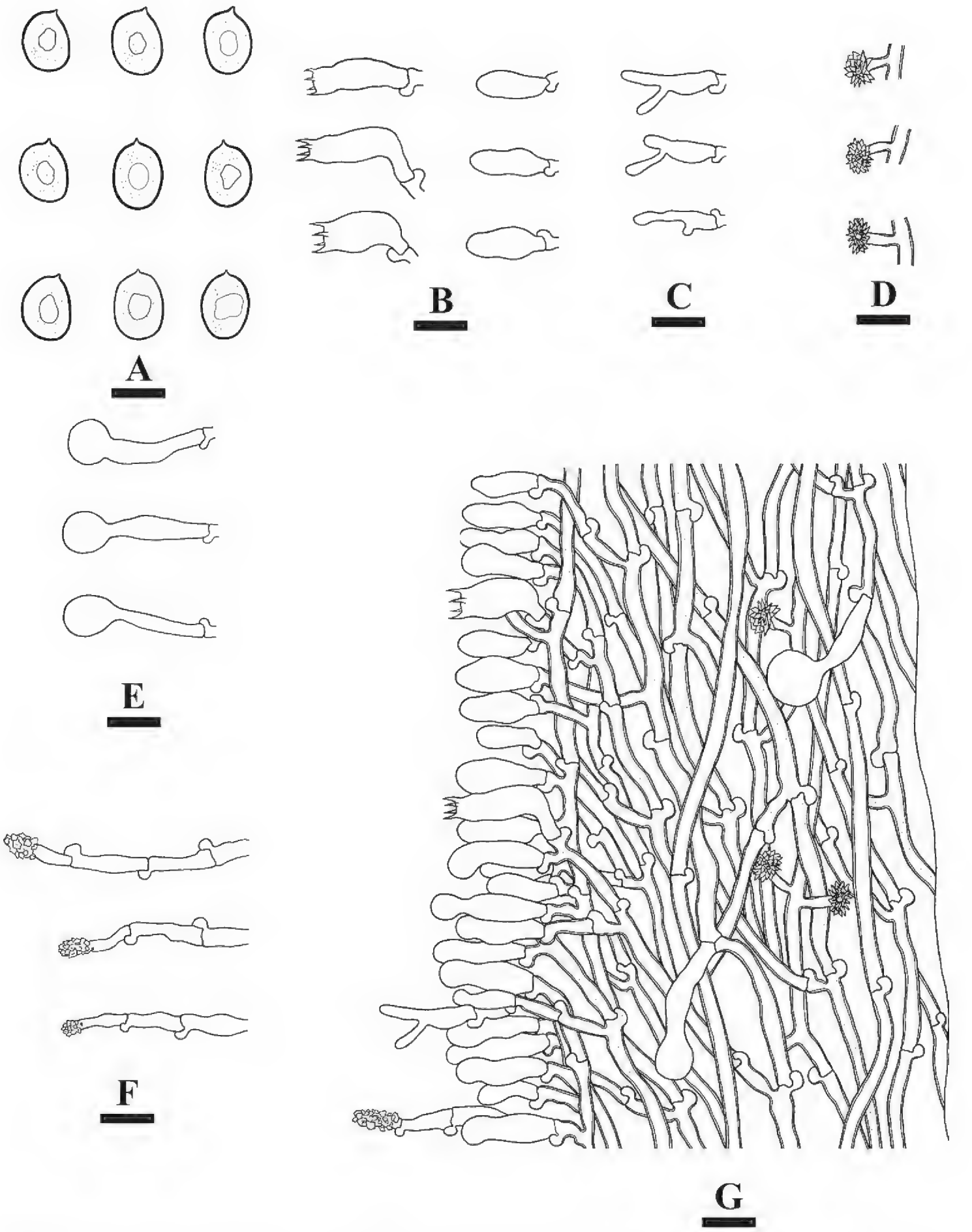

Figure 13. Microscopic structures of *Xylodon puerensis* (holotype) **A** basidiospores **B** basidia and basidioles **C** paraphysoid cystidia **D** astrocystidium **E** capitate cystidia **F** septocystidium cystidia **G** a section of hymenium. Scale bars: 5 μm (**A**); 10 μm (**B–G**).

Discussion

Many recently described wood-inhabiting fungal taxa have been reported in the subtropics and tropics, including in the genera *Lyomyces* and *Xylodon* (Xiong et al. 2009; Chen et al. 2017; Kan et al. 2017a, b; Riebesehl and Langer 2017; Viner et al. 2018; Chen and Zhao 2020; Luo et al. 2021a, b, c; Luo et al. 2022; Qu and Zhao 2022; Qu et al. 2022; Viner et al. 2022). Prior to this study, the following fourteen *Lyomyces* species were reported from China: *L. albus* (Sheng H. Wu) Riebesehl & Langer, *L. bambusinus*, *L. capitatocystidiatus* (H.X. Xiong, Y.C. Dai & Sheng H. Wu) Riebesehl & Langer, *L. cremeus* C.L. Zhao, *L. fissuratus*, *L. fumosus*, *L. leptocystidiatus* Xue W. Wang & L.W. Zhou, *L. macrosporus* C.L. Zhao & K.Y. Luo, *L. microfasciculatus* (Yurchenko & Sheng H. Wu) Riebesehl & Langer, *L. niveus*, *L. ochraceoalbus*, *L. sambuci*, *L. tenuissimus* (Yurchenko & Sheng H. Wu) Riebesehl & Langer and *L. wuliangshanensis* C.L. Zhao. (Xiong et al. 2009; Yurchenko et al. 2013; Riebesehl and Langer 2017; Chen and Zhao 2020; Luo et al. 2021b, c; Wang et al. 2021). The present study reports five new species in *Lyomyces* and *Xylodon*, based on a combination of morphological features and molecular evidence.

Phylogenetically, based on the multiple loci in *Hyphodontia* s.l., six genera, *Fasciodontia*, *Hastodontia*, *Hyphodontia*, *Lyomyces*, *Kneiffiella*, and *Xylodon*, were divided into four clades in the order Hymenochaetales (Wang et al. 2021). In the present study, based on the ITS+nLSU data (Fig. 1), *Lyomyces* and *Xylodon* were grouped with *Fasciodontia*, *Hastodontia*, *Hyphodontia* and *Kneiffielle*, in which five new species were grouped into the genera *Lyomyces* and *Xylodon*. Based on ITS topology (Figs 2, 3), *L. albopulverulentus* formed a monophyletic lineage, and was then grouped closely with *L. bambusinus*, *L. orientalis*, and *L. sambuci*. In addition, *L. yunnanensis* was found to be a sister to *L. niveus* with strong supports. The topology, based on ITS sequences, revealed that *X. daweishanensis* was retrieved as a sister to *X. hyphodontinus*. Moreover, *X. fissuratus* was grouped with the four taxa *X. montanus*, *X. subclavatus*, *X. wenshanensis*, and *X. xinpingensis*. *X. puerensis* was clustered with *X. flaviporus*, *X. ovisporus*, *X. subflaviporus*, *X. subtropicus*, and *X. taiwanianus*. However, morphologically, *L. bambusinus* can be delimited from *L. albopulverulentus* by its colliculose-to-tuberculate hymenial surface, its narrower basidia (16.5–35 × 3.5–7 μm), and its smaller and more broadly ellipsoid basidiospores (4.7–5.9 × 3.7–4.6 μm; Chen and Zhao 2020); Further, *L. orientalis* can be delimited from *L. albopulverulentus* by its smooth or slightly tuberculate hymenial surface, and by both its smaller basidia (13–20 × 3.5–4.5 μm) and basidiospores (5–6 × 4–4.5 μm; Yurchenko et al. 2017); *L. sambuci* can be delimited from *L. albopulverulentus* by its smooth-to-tuberculate hymenial surface and its smaller basidiospores (4.5–6 × 3.5–4 μm; Bernicchia and Gorjón 2010); *L. niveus* can be delimited from *L. yunnanensis* by a smaller basidia (9.5–15.0 × 3.5–5.5 μm) and broadly ellipsoid basidiospores (3.5–5 × 3–4 μm; Luo et al. 2021c). *Xylodon hyphodontinus* differs from *X. daweishanensis* by its larger basidiospores (4–5 × 4.5 μm; Hjortstam and Ryvarden 1980). *X. montanus* could be delimited from *X. fissuratus* by its smooth hymenial surface and moniliform cystidia (19.5–47.6 × 3.6–7.1 μm; Qu et al. 2022);

X. subclavatus differs from *X. fissuratus* by its larger capitate cystidia (20–25 × 3–4 μm) and wider basidiospores (4–5.5 × 3.5–4; Yurchenko et al. 2013); *X. wenshanensis* can be delimited from *X. fissuratus* by its smaller capitate cystidia (6–11 × 3–6.5 μm; Luo et al. 2022); *X. xinpingensis* can be delimited from *X. fissuratus* by its reticulate hymenial surface and larger basidia (18.5–33 × 3–6.5 μm; Ma and Zhao 2021). *Xylodon flaviporus* differs from *X. puerensis* by its wider basidia (14.5–20 × 5–7 μm) and smaller basidiospores (4.5–5.5 × 3–3.5 μm; Ryvarden 1985); *X. ovisporus* differs from *X. puerensis* by its smaller basidiospores (3.5–4.3 × 2.8–3.3 μm; Riebesehl and Langer 2017); *X. subflaviporus* is distinguishable from *X. puerensis* by its narrower basidia (8–18 × 4–5 μm) and smaller basidiospores (3.9–4.8 × 2.7–3.5 μm; Chen et al. 2017); *X. subtropicus* differs from *X. puerensis* by its smaller basidiospores (5–5.8 × 3.5–4 μm; Chen et al. 2017); *X. taiwanianus* differs from *X. puerensis* by its smaller basidiospores (4.5–5.5 × 2.6–3 μm; Wu 2001).

Morphologically, *Lyomyces albopulverulentus* resembles *L. bambusinus*, *L. cremeus*, *L. mascarensis* Riebesehl, Yurch. & Langer, *L. orientalis*, and *L. wuliangshanensis*, by sharing capitate cystidia and ellipsoid basidiospores. However, *L. bambusinus* differs from *L. albopulverulentus* by possessing a tapering cystidia (40–65 × 4–5.5 μm) and smaller basidiospores (4.7–5.9 × 3.7–4.6 μm; Chen and Zhao 2020); *L. cremeus* differs from *L. albopulverulentus* by its narrower capitate cystidia (20–40 × 3–5 μm), both smaller basidia (9–18.5 × 3–6 μm) and basidiospores (4.5–5.6 × 3.3–4.3 μm; Chen and Zhao 2020); *L. mascarensis* can be delimited from *L. albopulverulentus* by smaller capitate cystidia (17–38 × 3.5–6 μm), basidia (16–17.5 × 3.5–4.5 μm) and basidiospores (4.5–6 × 3.3–4 μm; Yurchenko et al. 2017); *L. orientalis* can be delimited from *L. albopulverulentus* due to its smaller capitate cystidia (17–38 × 3.5–6 μm), basidia (16–17.5 × 3.5–4.5 μm) and basidiospores (4.5–6 × 3.3–4 μm; Yurchenko et al. 2017); *L. wuliangshanensis* is different from *L. albopulverulentus* by smaller capitate cystidia (22–37 × 3–6 μm), basidia (12–20 × 3–4.3 μm) and basidiospores (3.5–5.3 × 2.8–4 μm; Chen and Zhao 2020).

Morphologically, *Lyomyces yunnanensis* resembles *L. bambusinus*, *L. cremeus*, *L. fumosus*, *L. fissuratus* and *L. wuliangshanensis* in both its capitate and tapering cystidia. However, *L. bambusinus* differs from *L. yunnanensis* by possessing a larger capitate cystidia (35–55 × 4–7 μm; Chen and Zhao 2020); *L. cremeus* differs from *L. yunnanensis* due to its smooth hymenial surface and smaller basidia (9–18.5 × 3–6 μm; Chen and Zhao 2020); *L. fissuratus* can be delimited from *L. yunnanensis* by its white-to-cream hymenial surface, and the presence of submoniliform cystidia (15.5–22 × 2.7–4 μm; Luo et al. 2021b); *L. fumosus* differs from *L. yunnanensis* due to its smooth hymenial surface, the presence of moniliform cystidia (8.5–22.7 × 2.5–3.7 μm), and its smaller basidia (11.5–17.5 × 3–5 μm; Luo et al. 2021b); *L. wuliangshanensis* is distinguishable from *L. yunnanensis* by its larger capitate cystidia (22–37 × 3–6 μm) and its smaller basidiospores (3.5–5.3 × 2.8–4 μm; Chen and Zhao 2020).

Morphologically, *Xylodon daweishanensis* is similar to *X. follis* Riebesehl et al., *X. grandineus* K.Y. Luo & C.L. Zhao, *X. laceratus* C.L. Zhao, *X. macrosporus*, *X. sinensis* C.L. Zhao & K.Y. Luo and *X. tropicus* C.L. Zhao due to its grandinioid,

or odontioid, hymenial surface. However, *X. follis* differs from *X. daweishanensis* due to its cream hymenial surface, wider capitate cystidia (17–30 × 4.5–9 μm), and larger, globose to subglobose basidiospores (8–9.5 × 7–8.5 μm; Riebesehl et al. 2019); *X. grandineus* differs from *X. daweishanensis* by its subulate cystidia (11–19 × 3–5 μm; Luo et al. 2022); *X. laceratus* can be delimited from *X. daweishanensis* by its fusiform cystidia (20.3–26.8 × 5.3–6.4 μm) and its larger basidiospores (3.9–5.3 × 2.6–4.1 μm; Qu et al. 2022); *X. macrosporus* differs from *X. daweishanensis* by its cylindrical cystidia (44–79.5 × 3–6 μm), larger basidia (11.5–36 × 5–11 μm) and thick-walled basidiospores (8–10.5 × 7.5–9 μm; Luo et al. 2021a); *X. sinensis* differs from *X. daweishanensis* by its fusiform cystidia (10–21 × 3–6 μm), and its buff-to-brown hymenial surface (Luo et al. 2021a); *X. tropicus* can be delimited from *X. daweishanensis* by its subglobose, slightly thick-walled basidiospores (Qu et al. 2022).

Xylodon fissuratus resembles *X. attenuatus* Spirin & Viner, *X. borealis* (Kotir. & Saaren.) Hjortstam & Ryvarden, *X. bresinskyi* (Langer) Hjortstam & Ryvarden, *X. dimiticus* (Jia J. Chen & L.W. Zhou) Riebesehl & E. Langer, *X. grandineus* and *X. vesiculosus* Yurchenko et al. by it sharing similar ellipsoid basidiospores. However, *X. attenuatus* differs from *X. fissuratus* due to its odontoid hymenial surface, the presence of hyphoid cystidia (17.6–39 × 2.7–4.6 μm) and its larger capitate cystidia (14.2–27.2 × 3.3–4.5 μm; Viner et al. 2018); *X. borealis* differs from *X. fissuratus* by its slender hypha-like cystidia (40–70 × 3–5 μm), larger capitate cystidia (20–50 × 4–6 μm) and basidia (15–20 × 4–5 μm; Bernicchia and Gorjón 2010); *X. bresinskyi* differs from *X. fissuratus* by its poroid hymenial surface with rudimentary console shaping (Langer 2000); *X. dimiticus* is distinguishable from *X. fissuratus* by poroid hymenial surface with angular pores (2–4 per mm; Chen et al. 2016); *X. grandineus* differs from *X. fissuratus* due to its subulate cystidia (11–19 × 3–5 μm) and its smaller basidiospores (3–4.5 × 2–3 μm; Luo et al. 2022); *X. vesiculosus* can be delimited from *X. fissuratus* by its odontioid hymenial surface and larger basidiospores (5.3–6.3 × 3–4 μm; Riebesehl et al. 2019).

Xylodon puerensis is similar to *X. bresinskyi*, *X. dimiticus*, *X. hallenbergii* (Sheng H. Wu) Hjortstam & Ryvarden, *X. poroideoefibulatus* (Sheng H. Wu) Hjortstam & Ryvarden, *X. reticulatus* (C.C. Chen & Sheng H. Wu) C.C. Chen & Sheng H. Wu, *X. subtropicus* and *X. syringae* (Langer) Hjortstam & Ryvarden by sharing a similar poroid hymenophore. However, *X. bresinskyi* can be delimited from *X. puerensis* by possessing smaller basidiospores (4.5–5.5 × 3–3.5 μm; Langer 2000); *X. dimiticus* differs from *X. puerensis* by possessing smaller basidia (9–13 × 4.5–6 μm) and basidiospores (3.8–4.6 × 2.8–3.5 μm; Chen et al. 2016); *X. hallenbergii* can be delimited from *X. fissuratus* by its both smaller capitate cystidia (15–23 × 4–5.3 μm) and basidiospores (4.2–5 × 4–4.3 μm; Wu 2001); *X. poroideoefibulatus* differs from *X. puerensis* by possessing smaller capitate cystidia (12–23 × 5.5–6.5 μm) and basidiospores (5–5.7 × 4–4.5 μm; Wu 2001); *X. reticulatus* can be delimited from *X. puerensis* by possessing smaller basidiospores (5–5.5 × 3.5–4 μm; Wu 1990); *X. syringae* differs from *X. puerensis* by its larger basidia (20–32 × 4–5 μm) and suballantoid basidiospores (8–9 × 3–3.5 μm; Hjortstam and Ryvarden 2009).

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References

Bernicchia A, Gorjón SP (2010) Fungi Europaei 12: Corticiaceae s.l. Edizioni Candusso, Alassio, Italy, 1008 pp.

Chen JZ, Zhao CL (2020) Morphological and molecular identification of four new resupinate species of *Lyomyces* (Hymenochaetales) from southern China. MycoKeys 65: 101–118. https://doi.org/10.3897/mycokeys.65.48660

Chen JJ, Zhou LW, Ji XH, Zhao CL (2016) *Hyphodontia dimitica* and *H. subefibulata* spp. nov. (Schizoporaceae, Hymenochaetales) from southern China based on morphological and molecular characters. Phytotaxa 269: 001–013. https://doi.org/10.11646/phytotaxa.269.1.1

Chen CC, Wu SH, Chen CY (2017) Three new species of *Hyphodontia* s.l. (Basidiomycota) with poroid or raduloid hymenophore. Mycological Progress 16(5): 553–564. https://doi.org/10.1007/s11557-017-1286-0

Chevallier FF (1826) Flore Générale des Environs de Paris. Ferra Jeune, Paris, 674 pp.

Cui BK, Li HJ, Ji X, Zhou JL, Song J, Si J, Yang ZL, Dai YC (2019) Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. Fungal Diversity 97(1): 137–392. https://doi.org/10.1007/s13225-019-00427-4

Cunningham GH (1959) Hydnaceae of New Zealand. Part II. The genus *Odontia*. Transactions of the Royal Society of New Zealand 86: 65–103.

Cunningham GH (1963) The Thelephoraceae of Australia and New Zealand. Bulletin of the New Zealand Department of Scientific and Industrial Research 145: 1–359.

Dai YC (2010) Hymenochaetaceae (Basidiomycota) in China. Fungal Diversity 45(1): 131–343. https://doi.org/10.1007/s13225-010-0066-9

Dai YC (2011) A revised checklist of corticioid and hydnoid fungi in China for 2010. Mycoscience 52(1): 69–79. https://doi.org/10.1007/S10267-010-0068-1

Dai YC (2012) Polypore diversity in China with an annotated checklist of Chinese polypores. Mycoscience 53(1): 49–80. https://doi.org/10.1007/s10267-011-0134-3

Dai YC, Yang ZL, Cui BK, Wu G, Yuan HS, Zhou LW, He SH, Ge ZW, Wu F, Wei YL, Yuan Y, Si J (2021) Diversity and systematics of the important macrofungi in Chinese forests. Junwu Xuebao 40: 770–805.

Felsenstein J (1985) Confidence intervals on phylogenetics: An approach using bootstrap. Evolution. International Journal of Organic Evolution 39(4): 783–791. https://doi.org/10.2307/2408678

Gafforov Y, Riebesehl J, Ordynets A, Langer E, Yarasheva M, Ghobad-Nejhad M, Zhou L-W, Wang X-W, Gugliotta AM (2017) *Hyphodontia* (Hymenochaetales, Basidiomycota) and similar taxa from Central Asia. Botany 95(11): 1041–1056. https://doi.org/10.1139/cjb-2017-0115

Girometta CE, Bernicchia A, Baiguera RM, Bracco F, Buratti S, Cartabia M, Picco AM, Savino E (2020) An italian researchculture collection of wood decay fungi. Diversity (Basel) 12(2): 58. https://doi.org/10.3390/d12020058

Gray SF (1821) A Natural Arrangement of British Plants. Nabu Press, London, UK, 649 pp.

Greslebin AG, Rajchenberg M (2000) The genus *Hyphodontia* in the Patagonian Andes Forest of Argentina. Mycologia 92(6): 1155–1165. https://doi.org/10.1080/00275514.2000.12061263

He SH, Li HJ (2013) *Pseudochaete latesetosa* and *P. subrigidula* spp. nov. (Hymenochaetales, Basidiomycota) from China based on morphological and molecular characters. Mycological Progress 12(2): 331–339. https://doi.org/10.1007/s11557-012-0838-6

Hjortstam K, Ryvarden L (1980) Studies in tropical Corticiaceae (Basidiomycetes). II. Mycotaxon 12: 168–184.

Hjortstam K, Ryvarden L (2007) Studies in corticioid fungi from Venezuela III (Basidiomycotina, Aphyllophorales). Synopsis Fungorum 23: 56–107.

Hjortstam K, Ryvarden L (2009) A checklist of names in *Hyphodontia* sensu stricto-sensu lato and *Schizopora* with new combinations in *Lagarobasidium*, *Lyomyces*, *Kneiffiella*, *Schizopora*, and *Xylodon*. Synopsis Fungorum 26: 33–55.

Hyde KD (2022) The numbers of fungi. Fungal Diversity 114(1): 1. https://doi.org/10.1007/s13225-022-00507-y

James TY, Stajich JE, Hittinger CT, Rokas A (2020) Toward a fully resolved fungal tree of life. Annual Review of Microbiology 74(1): 291–313. https://doi.org/10.1146/annurev-micro-022020-051835

Jiang N, Voglmayr H, Bian DR, Piao CG, Wnag SK, Li Y (2021) Morphology and phylogeny of *Gnomoniopsis* (Gnomoniaceae, Diaporthales) from fagaceae leaves in China. Journal of Fungi (Basel, Switzerland) 7(10): 792. https://doi.org/10.3390/jof7100792

Kan YH, Gafforov Y, Li T, Zhou LW (2017a) *Hyphodontia zhixiangii* sp. nov. (Schizoporaceae, Basidiomycota) from Uzbekistan. Phytotaxa 299(2): 273–279. https://doi.org/10.11646/phytotaxa.299.2.12

Kan YH, Qin WM, Zhou LW (2017b) *Hyphodontia mollissima* sp. nov. (Schizoporaceae, Hymenochaetales) from Hainan, southern China. Mycoscience 58(4): 297–301. https://doi.org/10.1016/j.myc.2017.04.003

Karsten PA (1881) Enumeratio Thelephorearum Fr. et Clavariearum Fr. Fennicarum, systemate novo dispositarum. Revue Mycologique Toulouse 3: 21–23.

Karsten PA (1882) Rysslands, Finlands och den Skandinaviska halföns Hattsvampar. Sednare Delen: Pip-, Tagg-, Hud-, Klubboch Gelésvampar. Bidrag till Kännedom av Finlands Natur och. Folk (Kobenhavn) 37: 1–257.

Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20(4): 1160–1166. https://doi.org/10.1093/bib/bbx108

Kotiranta H, Saarenoksa R (2000) Three new species of *Hyphodontia* (Coritciaceae). Annales Botanici Fennici 37(4): 255–278.

Kuntze OI (1898) Revisio Generum Plantarum. A. Felix, Leipzig, Germany, 576 pp.

Langer E (1994) Die Gattung *Hyphodontia* John Eriksson. Bibliotheca Mycologica, Schweizerbart Science Publishers, Stuttgart, Germany, Volume 154, 298 pp.

Langer E (2000) Bemerkenswerte pilze aus dem Nationalpark Bayerischer Wald: *Schizopora bresinskyi* sp. nov. Hoppea 61: 229–235.

Larsson KH (2007) Re-thinking the classification of corticioid fungi. Mycological Research 111(9): 1040–1063. https://doi.org/10.1016/j.mycres.2007.08.001

Larsson A (2014) AliView: A fast and lightweight alignment viewer and editor for large data sets. Bioinformatics 30(22): 3276–3278. https://doi.org/10.1093/bioinformatics/btu531

Larsson KH, Larsson E, Kõljalg U (2004) High phylogenetic diversity among corticioid homobasidiomycetes. Mycological Research 108(9): 983–1002. https://doi.org/10.1017/S0953756204000851

Larsson KH, Parmasto E, Fischer M, Langer E, Nakasone KK, Redhead SA (2006) Hymenochaetales: A molecular phylogeny for the hymenochaetoid clade. Mycologia 98(6): 926–936. https://doi.org/10.1080/15572536.2006.11832622

Lee IS, Langer E (2012) New records of *Hyphodontia* species from Taiwan. Nova Hedwigia 94(1–2): 239–244. https://doi.org/10.1127/0029-5035/2012/0094-0239

Luo KY, Zhao CL (2021) *Fasciodontia yunnanensis* (Schizoporaceae, Hymenochaetales), a new species from southern China. Annales Botanici Fennici 58(4–6): 259–266. https://doi.org/10.5735/085.058.0411

Luo KY, Qu MH, Zhao CL (2021a) Additions to the knowledge of Corticioid *Xylodon* (Schizoporaceae, Hymenochaetales): Introducing three new *Xylodon* species from southern China. Diversity (Basel) 13(11): 581. https://doi.org/10.3390/d13110581

Luo X, Chen YH, Zhao CL (2021b) *Lyomyces fissuratus* and *L. fumosus* (Schizoporaceae, Hymenochaetales), new species from southern China. Annales Botanici Fennici 4(4–6): 58. https://doi.org/10.5735/085.058.0404

Luo X, Chen YH, Zhao CL (2021c) Morphological and phylogenetic characterization of fungi within Hymenochaetales: Introducing two new species from southern China. Nordic Journal of Botany 12(12): 39. https://doi.org/10.1111/njb.03414

Luo KY, Chen ZY, Zhao CL (2022) Phylogenetic and taxonomic analyses of three new wood-inhabiting Fungi of *Xylodon* (Basidiomycota) in a Forest Ecological System. Journal of Fungi (Basel, Switzerland) 8(4): 405. https://doi.org/10.3390/jof8040405

Ma X, Zhao CL (2021) *Xylodon bambusinus* and *X. xinpingensis* spp. nov. (Hymenochaetales) from southern China. Phytotaxa 511(3): 231–247. https://doi.org/10.11646/phytotaxa.511.3.3

Miller MA, Pfeiffer W, Schwartz T (2012) The CIPRES Science Gateway: Enabling high-impact science for phylogenetics researchers with limited resources. Association for Computing Machinery 39: 1–8. https://doi.org/10.1145/2335755.2335836

Nylander JAA (2004) MrModeltest v.2. Program Distributed by the Author; Evolutionary Biology Centre, Uppsala University, Uppsala, Sweden.

Paulus B, Hallenberg N, Buchanan PK, Chambers GK (2000) A phylogenetic study of the genus *Schizopora* (Basidiomycota) based on ITS DNA sequences. Mycological Research 104(10): 1155–1163. https://doi.org/10.1017/S0953756200002720

Petersen JH (1996) The Danish Mycological Society's colour-chart. Foreningen til Svampekundskabens Fremme, Greve.

Qu MH, Zhao CL (2022) *Xylodon flocculosus* sp. nov. from Yunnan, China. Mycotaxon 137(2): 189–201. https://doi.org/10.5248/137.189

Qu MH, Wang DQ, Zhao CL (2022) A phylogenetic and taxonomic study on *Xylodon* (Hymenochaetales): Focusing on three new *Xylodon* species from southern China. Journal of Fungi (Basel, Switzerland) 8(1): 35. https://doi.org/10.3390/jof8010035

Rabenhorst GL (1851) Klotzschii herbarium vivum mycologicum sistens fungorum per totam Germaniam crescentium collectionem perfectam. Editio prima. Centuria 8: 1501–1600.

Rehner SA, Samuels GJ (1994) Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. Mycological Research 98(6): 625–634. https://doi.org/10.1016/S0953-7562(09)80409-7

Riebesehl J, Langer E (2017) *Hyphodontia* s.l. (Hymenochaetales, Basidiomycota): 35 new combinations and new keys to currently all 120 species. Mycological Progress 16(6): 637–666. https://doi.org/10.1007/s11557-017-1299-8

Riebesehl J, Yurchenko E, Nakasone KK, Langer E (2019) Phylogenetic and morphological studies in *Xylodon* (Hymenochaetales, Basidiomycota) with the addition of four new species. MycoKeys 47: 97–137. https://doi.org/10.3897/mycokeys.47.31130

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Ryvarden L (1985) Type studies in the Polyporaceae 17. Species described by W.A. Murrill. Mycotaxon 23: 169–198.

Shi ZW, Wang XW, Zhou LW, Zhao CL (2019) *Xylodon kunmingensis* sp. nov. (Hymenochaetales, Basidiomycota) from southern China. Mycoscience 60(3): 184–188. https://doi.org/10.1016/j.myc.2019.02.002

Tura DA, Zmitrovich IV, Wasser SP, Spirin WA, Nevo E (2011) Biodiversity of the Heterobasidiomycetes and Non-Gilled Hymenomycetes (Former Aphyllophorales) of Israel. ARA Gantner Verlag K-G, Ruggell, Liechtenstein, 566 pp.

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172(8): 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

Viner I, Spirin V, Zíbarová L, Larsson KH (2018) Additions to the taxonomy of *Lagarobasidium* and *Xylodon* (Hymenochaetales, Basidiomycota). MycoKeys 41: 65–90. https://doi.org/10.3897/mycokeys.41.28987

Viner I, Bortnikov F, Miettinen O (2022) On six African species of *Lyomyces* and *Xylodon*. Fungal Systematics and Evolution 8: 163–178. https://doi.org/10.3114/fuse.2021.08.13

Vu D, Groenewald M, Vries M, Gehrmann T, Stielow B, Eberhardt U (2019) Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom Fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology 92(1): 135–154. https://doi.org/10.1016/j.simyco.2018.05.001

Wang M, Chen YY (2017) Phylogeny and taxonomy of the genus *Hyphodontia* (Hymenochaetales, Basidiomycota) in China. Phytotaxa 309(1): 45–54. https://doi.org/10.11646/phytotaxa.309.1.4

Wang XW, May TW, Liu SL, Zhou LW (2021) Towards a natural classification of *Hyphodontia* sensu lato and the trait evolution of basidiocarps within Hymenochaetales (Basidiomycota). Journal of Fungi (Basel, Switzerland) 7(6): 478. https://doi.org/10.3390/jof7060478

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR protocols: A Guide to Methods And Applications. Academic Press, San Diego, CA, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wijayawardene NN, Hyde KD, Al-Ani LKT, Tedersoo L, Haelewaters D, Rajeshkumar KC, et al. (2020) Outline of Fungi and fungus-like taxa. Mycosphere 11(1): 1060–1456. https://doi.org/10.5943/mycosphere/11/1/8

Wu SH (1990) The Corticiaceae (Basidiomycetes) subfamilies Phlebioideae, Phanerochaetoideae and Hyphodermoideae in Taiwan. Acta Botanica Fennica 142: 1–123.

Wu SH (2000) Studies on *Schizopora flavipora* s.l., with special emphasis on specimens from Taiwan. Mycotaxon 76: 51–66.

Wu SH (2001) Three new species of *Hyphodontia* with poroid hymenial surface. Mycologia 93(5): 1019–1025. https://doi.org/10.1080/00275514.2001.12063235

Wu SH (2006) *Hyphodontia tubuliformis*, a new species from Taiwan. Mycotaxon 95: 185–188.

Wu F, Zhou LW, Vlasák J, Dai YC (2022a) Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. Fungal Diversity 113(1): 1–192. https://doi.org/10.1007/s13225-021-00496-4

Wu F, Man XW, Tohtirjap A, Dai YC (2022b) A comparison of polypore fungal and species composition in forest ecosystems of China, North America, and Europe. Forest Ecosystems 9: 100051. https://doi.org/10.1016/j.fecs.2022.100051

Xiong HX, Dai YC, Wu SH (2009) Three new species of *Hyphodontia* from Taiwan. Mycological Progress 8(3): 165–169. https://doi.org/10.1007/s11557-009-0587-3

Xiong HX, Dai YC, Wu SH (2010) Two new species of *Hyphodontia* from China. Mycologia 102(4): 918–922. https://doi.org/10.3852/09-139

Yurchenko E, Wu SH (2013) Three new species of *Hyphodontia* with peg-like hyphal aggregations. Mycological Progress 13(3): 533–545. https://doi.org/10.1007/s11557-013-0935-1

Yurchenko E, Wu SH (2014) *Hyphoderma formosanum* sp. nov. (Meruliaceae, Basidiomycota) from Taiwan. Sydowia 66: 19–23.

Yurchenko E, Wu SH (2016) A key to the species of *Hyphodontia* sensu lato. MycoKeys 12: 1–27. https://doi.org/10.3897/mycokeys.12.7568

Yurchenko E, Xiong HX, Wu SH (2013) Four new species of *Hyphodontia* (*Xylodon* ss. Hjortstam & Ryvarden, Basidiomycota) from Taiwan. Nova Hedwigia 96(3–4): 545–558. https://doi.org/10.1127/0029-5035/2013/0092

Yurchenko E, Riebesehl J, Langer E (2017) Clarification of *Lyomyces sambuci* complex with the descriptions of four new species. Mycological Progress 16(9): 865–876. https://doi.org/10.1007/s11557-017-1321-1

Yurchenko E, Riebesehl J, Langer E (2020) *Fasciodontia* gen. nov. (Hymenochaetales, Basidiomycota) and the taxonomic status of *Deviodontia*. Mycological Progress 19(2): 171–184. https://doi.org/10.1007/s11557-019-01554-7

Zhao CL, Wu ZQ (2017) *Ceriporiopsis kunmingensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. Mycological Progress 16(1): 93–100. https://doi.org/10.1007/s11557-016-1259-8

Zhao CL, Cui BK, Dai YC (2014) Morphological and molecular identification of two new species of *Hyphodontia* (Schizoporaceae, Hymenochaetales) from southern China. Cryptogamie. Mycologie 35(1): 87–97. https://doi.org/10.7872/crym.v35.iss1.2014.87